

What is claimed is:

1. A method of assigning an individual to a population of origin, which comprises:

(a) identifying a set of candidate populations of origin, wherein each candidate population is characterized by genotype frequencies and allele frequencies at one or more marker loci;

(b) determining a population prior genotype probability for each individual and candidate population of origin using knowledge concerning the individual which is available prior to genotyping the individual;

(c) genotyping the individual to identify the alleles at one or more of the marker loci identified in step (a) to thereby identify the individual's genotype;

(d) based on the identified genotype of the individual, sequentially determining a population genotype probability for each candidate population of origin under a null hypothesis that the individual arose from the population;

(e) combining the population prior genotype probability from step (b) and the population genotype probability from step

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- (d) to obtain a population posterior genotype probability for each candidate population of origin;
- 5 (f) identifying a most likely population of origin wherein the population has the largest posterior genotype probability among the set of candidate populations; and
- 10 (g) assigning the individual to the population identified in step (f).
2. The method of claim 1, wherein the individual is only assigned to the most likely population of origin if the posterior genotype probability for the most likely population of origin exceeds a threshold value.
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3. The method of claim 1, which further comprises:
- 20 (a) computing a probability with which genotypes rarer than the individual's genotype occur in the most likely population of origin; and
- 25 (b) if the probability in step (a) is above a threshold value, assigning the individual to the population of origin previously identified as the most likely population of origin, or if the probability in step (a) is not above a threshold value, assigning the individual to a novel population that
- 30 is not represented among the set of

candidate populations of origin.

4. The method of claim 2, wherein the threshold value is determined empirically.

5. The method of claim 4, wherein the threshold value is determined using a sample of individuals from each candidate population who are independent of individuals used to characterize each candidate population.

6. The method of claim 4, wherein the threshold value is varied to determine the percentage of individuals who a) cannot be classified to a population of origin, b) are correctly classified, and c) are incorrectly classified.

7. The method of claim 3, wherein the threshold value is determined empirically.

8. The method of claim 7, wherein the threshold value is determined using a sample of individuals from each candidate population who are independent of individuals used to characterize each candidate population.

9. The method of claim 7, wherein the threshold value is varied to reduce the percentage of individuals who are incorrectly classified to a population.

10. The method of claim 1, wherein the population prior genotype probability is based on one or

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more morphological features of the individual.

11. The method of claim 10, wherein one or more morphological features allow the exclusion of one or more candidate populations of origin.

12. The method of claim 11, wherein one or more morphological features are selected from the group consisting of coat color, presence or absence of horns, presence or absence of a shoulder hump, and presence or absence of a long, downswept ear.

13. The method of claim 12, wherein the coat color is black or nonblack.

14. The method of claim 1, wherein the population prior genotype probability is set to equal a proportion of total population size that comprises each candidate population of origin.

15. The method of claim 1, wherein the population prior genotype probability is assumed to be uniform for each candidate population of origin.

16. The method of claim 1, wherein marker locus genotypes for each candidate population of origin are in Hardy-Weinberg Equilibrium and Gametic Phase Equilibrium.

17. The method of claim 1, wherein marker locus genotypes for each candidate population of

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origin are not in Hardy-Weinberg Equilibrium or Gametic Phase Equilibrium.

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18. The method of claim 1, wherein the individual is an animal.

19. The method of claim 18, wherein the animal is a cow, a heifer, a steer, a bull, a bullock, a pig, a horse, a fish, a chicken, a duck, a lamb, a shrimp, an oyster, a mussel, or a shellfish.

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20. The method of claim 1, wherein the candidate population of origin is selected based on a desirable trait.

21. The method of claim 20, wherein the desirable trait is selected from the group consisting of one or more of animal growth, quality grade, yield grade, marbling, rib-eye muscle area, dressing percentage, meat tenderness, meat flavor, meat palatability, fatness, fat color, unsaturated fatty acid content of fat, reproductive efficiency, prolificacy, disease resistance, feed conversion efficiency, drought tolerance, and heat tolerance.

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22. The method of claim 1, wherein the candidate population of origin is selected based on an undesirable trait.

23. The method of claim 22, wherein the undesirable trait is toughness of meat.